



JOURNAL Unpublished  
2 (bases 1 to 185839)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
COMMENT -----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
-----  
Project Information  
Center Project Name: 1909420  
Center clone name: RPCT-23\_449F12  
-----  
Summary Statistics  
Consensus quality: 172503 bases at least 040  
Consensus quality: 177768 bases at least 030  
Consensus quality: 170703 bases at least 020  
Estimated insert size: 187000; agarose-fp estimation  
Estimated insert size: 184339; sum-of-contigs estimation  
Quality coverage: 7.81 in 020 bases; agarose-fp estimation  
Quality coverage: 7.93 in 020 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 1081: contig of 1081 bp in length  
\* 1181: gap of unknown length  
\* 4298: contig of 3117 bp in length  
\* 4298: gap of unknown length  
\* 4399: 6732: contig of 2334 bp in length  
\* 6733: 6832: gap of unknown length  
\* 6832: 11726: contig of 4794 bp in length  
\* 11726: gap of unknown length  
\* 11727: 15445: contig of 3819 bp in length  
\* 15445: gap of unknown length  
\* 15646: 20007: contig of 4362 bp in length  
\* 20007: 26156: contig of 6049 bp in length  
\* 26156: gap of unknown length  
\* 26157: 20256: gap of unknown length  
\* 20256: 32958: contig of 6702 bp in length  
\* 32959: 33059: gap of unknown length  
\* 33059: 42014: contig of 8956 bp in length  
\* 42015: 42115: gap of unknown length  
\* 50689: 50788: gap of unknown length  
\* 61298: 61398: contig of 10510 bp in length  
\* 61398: gap of unknown length  
\* 61399: 77269: contig of 15871 bp in length  
\* 77270: 77369: gap of unknown length  
\* 77370: 95693: contig of 18324 bp in length  
\* 95693: gap of unknown length  
\* 95794: 119999: contig of 24206 bp in length  
\* 120099: gap of unknown length  
\* 120100: 15073: contig of 30174 bp in length  
\* 15073: 15074: gap of unknown length  
\* 15074: 150373: gap of 35466 bp in length.  
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/clone\_id="43498"  
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BASE COUNT  
48719 a 43498 c 42466 g 49655 t 1501 others  
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Query Match Local Similarity 90.4%; Score 592.8; DB 2; Length 185839;  
Best Local Similarity 95.3%; Pred. No. 2.7e-127; Pred. No. 2.7e-127;  
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QY	61	TGGCCCTCTAGGGCCCCCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120			
Db	57527	TGGCCCTCTAGGGCCCCCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	57468			
QY	121	CCGGCCCTCGCTGCCCGTGGGGGCCAACGGCCCCGGTCCAGGTGAACTGG	180			
Db	57467	CCCGCCCTCGCTGCCCGTGGGGGCCAACGGCCCCGGTCCAGGTGAACTGG	57408			
QY	181	AGTCATTTGAAACGCTGGAATGAGAGAGGGTTGGGTGAAAGGGGTTGAGGAC	240			
Db	57407	AGTCATTTGAAACGCTGGAATGAGAGAGGGTTGGGTGAAAGGGGTTGAGGAC	57348			
QY	241	TACTGACCACATCGGCCGCTCGGGCTGAGCTCGCTGAGGAGCTACAGCAGC	300			
Db	57347	TACTGACCACATCGGCCGCTCGGGCTGAGCTCGCTGAGGAGCTACAGCAGC	57288			
QY	301	ACTACTGGCTCTACAACAAGCTCATCTGCAACACCAACACTCACAGCAGTG	360			
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QY	361	ACGGACACCCCATGGGGGACTGGCTCTCGAGAGAGAACCTCACAGCAGTG	420			
Db	57227	ACGGACACCCCATGGGGGACTGGCTCTCGAGAGAGAACCTCACAGCAGTG	57168			
QY	421	CACATTCAGGCTCTGGGCGATATGCTGCTGGAGGTAGGGTCAGGAGGCCCTGG	480			
Db	57167	CACATTCAGGCTCTGGGCGATATGCTGCTGGAGGTAGGGTCAGGAGGCCCTGG	57108			
QY	481	GGCACACCTCGCTGAGCCCTGCTCTGAGCTGAGCTTACTGCTGGAGGGCTN	540			
Db	57107	GGCACACCTCGCTGAGCCCTGCTCTGAGCTGAGCTTACTGCTGGAGGGCTN	57048			
QY	541	CCCAAGGNCCTGAGGGCTGCTCTGAGCTGAGCTTACTGCTGGAGGGCTN	600			
Db	57047	CCCAAGGCTCTGAGGGCTGCTCTGAGCTGAGCTTACTGCTGGAGGGCTN	56988			
QY	601	TNCCTNTNTAAATCCCTCTCTGGGATNTNTGTTATTTTCTTTCTTG	656			
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RESULT 2

	LOCUS	AC11434/C
DEFINITION	Rattus norvegicus clone CH230-210C18, *** SEQUENCING IN PROGRESS	
ACCESSION	AC114434	
VERSION	AC114434.2	GI:21737492
KEYWORDS		
SOURCE	Rattus norvegicus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 18910)	
AUTHORS	Muzny, D. M., Adams, C., Adio-oduoala, B., Ali-osman, F. R., Allen, C., Alsbrooks, S. L., Amaralungu, H. C., Are, J. R., Ayele, M., Banks, T., Barbara, J. J., Benton, J., Bimage, K., Blakenburg, K., Bonnici, D. P., Bouch, J., Bowie, S., Brileva, M., Brown, M., Bryant, N. P., Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J. J., Chevrel, D., Chen, G., Chen, Z., Chodury, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., Davis, M. L., Davis, C. C., Davy-Carroll, L., Dederich, D. A., Delaney, K. R., Delgado, O., Benn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C. C., Elhai, C., Escalante, M.,	

Falls, T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,R., Garner,T., Garza,N., Gill,R., Goralski,J.H., Guevara,W., Guaratino,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlik,P., Hayes,A., Hernandez,J., Hernández,O., Hodgson,A., Hoores,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,J.U., King,L., Kovar,C., Krautovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W., Loulsedg,H., Loxado,R.J., Lu,X., Luctier,A., Luctier,R., Luna,R., Ma,J., Maneshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mauthner,E., McLeod,M.P., Meadow,M., Miner,G., Miner,Z., Mitchell,T., Mohabut,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,N., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokonwo,S., Oguh,M., Okwuonu,G., Oraquyno,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sison,I., Sodergren,E., Sonake,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Sutak,A., Tabor,P., Tamersis,A., Tamersis,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G., and Gibbs,R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 178910)  
 Worley,K.C.  
 Direct Submission  
 Submitted (09-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 178910)  
 ..... Genome Center  
 Direct Submission  
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Jul 12, 2002 this sequence version replaced g1.19310225.  
 ..... Center  
 Center project name: GPEK  
 Center clone name: CH230-210C18  
 Center contact: hgsc-help@bcm.tmc.edu/  
 Center project information  
 Center project name: GPEK  
 Center clone name: CH230-210C18  
 Center contact: hgsc-help@bcm.tmc.edu/  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye: 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 126357 bases at least 040  
 Consensus quality: 130383 bases at least 030  
 Consensus quality: 134610 bases at least 020  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see <http://www.hgsc.bcm.tmc.edu/docs/Genbank/draft-data.html>).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 60 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 1046: contig of 1046 bp in length  
 \* 1 1145: gap of unknown length  
 \* 1 2255: contig of 1109 bp in length  
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 4947 5046: gap of unknown length  
 5046 6176: contig of 1130 bp in length  
 6177 6276: gap of unknown length  
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KEYWORDS		Homo sapiens	
ORGANISM		Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 1386)	
AUTHORS		Chu,P.J., Robertson,H.M. and Best,P.M.	
TITLE		Calcium channel gamma subunits provide insights into the evolution of this gene family	
JOURNAL		Gene 280 (1-2), 37-48 (2001)	
MEDLINE		21601102	
PUBMED		11738816	
FEATURES		2 (bases 1 to 1386)	
source		Chu,P.J., Robertson,H. and Best,P.M.	
AUTHORS		Direct Submission	
TITLE		Submitted (14-MAR-2001) Department of Molecular and Integrative Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL 61801, USA	
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BASE COUNT		206 a 515 c 471 g 194 t	
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Query Match		35.4%; Score 232.2; DB 9; Length 1386;	
Best Local Similarity		78.3%; Pred. No. 1.4e-43;	
Matches		306; Conservative 0; Mismatches 78; Indels 7; Gaps 2;	
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Qy		133 TCCCCCGTGGCCACGGCCCGGGTGCAGGGTGAACCTGGGTATGAAAC 192	
Db		63 TCCCCGGATGATG-CCACGGCCCGGCTCCGGCTAACCTGGATGCTGAGC 121	
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Qy		367 CACCCCATGCTGGGGCTGCTGGAGAGAGGACCTGGGGCCCTGGGGCCCTCACGAT 426	
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RESULT		10	
REFERENCE		AF234892	
LOCUS		AF234892	
DEFINITION		Homo sapiens	
CDS		calcium channel gamma subunit 8 (CACNG8) mRNA, partial	
ORGANISM		Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 633)	
AUTHORS		Black,J.L. III, Kryzer,T.J. and Lennon,V.A.	
TITLE		Proposed Homo sapiens voltage-gated calcium channel gamma-6 subunit	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 633)	
AUTHORS		Black,J.L. III, Kryzer,T.J. and Lennon,V.A.	
TITLE		Submitted (15-FEB-2000) Department of Psychiatry and Psychology, Mayo Clinic, 200 SW 1st Street, Rochester, MN 55905, USA	
REFERENCE		1. 633	
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		/translation="GLNRPPGCVSLKRWNNEGLWCKKGVOVLTIVGAFAAFLGMLT	
		AISTDWKYLINTCNLTAFLGGDGSTPFRGGGASERKDDGGGATGCGTGCAGLWRCVKG	
		IKRGCVKINHPEDTDIDHSRKEILVRVRASSIFPLSATILLLUGGVCAVASRVKSKRVI	
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BASE COUNT		120 a 206 c 208 g 99 t	
ORIGIN			
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Best Local Similarity		82.0%; Pred. No. 4.9e-34;	
Matches		233; Conservative 0; Mismatches 48; Indels 3; Gaps 1;	
Qy		177 CTGGAGTATGGAAACGGCTGGAATGAGAGGGTGTGGTGAAGAGGGCTCAG 236	
Db		22 CAGGTGTCTGAGCGCCCTGGGGACGAGGGCTCAGGGGGCCCTCTGGGCCAG 81	
Qy		237 GTACTCTGAGCCATCTGGGGCTTCTGGGCTTCTGGGCTCTGGGCTCTGG 296	
Db		82 GAGCTGAGGAGCTGGGGGGCTCTGGGGGGCTCTGGGGGGCTCTGGGGGGCT 141	
Qy		297 ACTGACTCTGCTCATGAGGCTCTGGGGGGGGGGGGGGGGGGGGGGGGGG 353	
Db		142 ACTGACTCTGCTCATGAGGAGCTGGGGGGGGGGGGGGGGGGGGGGGGGG 201	
Qy		354 GTGTGAGTGGGGACCCATCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 413	
Db		202 GGGCGAGGGGGCCCCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 261	
Qy		414 GGCTTACACATCAGGGCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 457	
Db		262 GGCTTACACATCAGGGCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 305	



Consensus quality: 89224 bases at least Q20

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft'. It currently

\* consists of 67 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

1 1021: contig of 1021 bp in length  
 \* 1121: gap of unknown length  
 \* 1127: contig of 1176 bp in length  
 \* 2297: gap of unknown length  
 \* 2397: gap of 1416 bp in length  
 \* 3813: contig of 1416 bp in length  
 \* 3814: gap of unknown length  
 \* 3914: contig of 128 bp in length  
 \* 5197: gap of unknown length  
 \* 5297: contig of 1044 bp in length  
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 \* 6442: contig of 1305 bp in length  
 \* 7747: gap of unknown length  
 \* 7847: contig of 1807 bp in length  
 \* 9653: gap of unknown length  
 \* 9753: contig of 1678 bp in length  
 \* 11432: gap of unknown length  
 \* 11531: gap of unknown length  
 \* 11532: contig of 1265 bp in length  
 \* 12797: gap of unknown length  
 \* 12897: contig of 1163 bp in length  
 \* 14060: gap of unknown length  
 \* 14159: contig of 1118 bp in length  
 \* 15278: gap of unknown length  
 \* 15378: contig of 1046 bp in length  
 \* 16424: gap of unknown length  
 \* 16524: contig of 1592 bp in length  
 \* 18116: gap of unknown length  
 \* 18215: contig of 1130 bp in length  
 \* 19346: gap of unknown length  
 \* 19445: contig of 1796 bp in length  
 \* 21241: contig of 1823 bp in length  
 \* 21242: contig of unknown length  
 \* 21342: contig of 1155 bp in length  
 \* 22497: gap of unknown length  
 \* 22597: contig of 1257 bp in length  
 \* 23854: gap of unknown length  
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 \* 23954: contig of 1823 bp in length  
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 \* 27090: contig of 1089 bp in length  
 \* 27091: contig of 1131 bp in length  
 \* 28180: gap of unknown length  
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 \* 29411: gap of unknown length  
 \* 29511: contig of 1637 bp in length  
 \* 31147: gap of unknown length  
 \* 31247: contig of 1226 bp in length  
 \* 32474: gap of unknown length  
 \* 32573: contig of 2079 bp in length  
 \* 34653: contig of unknown length  
 \* 34753: gap of unknown length  
 \* 36601: contig of 1849 bp in length  
 \* 36701: gap of unknown length  
 \* 36702: contig of 1424 bp in length  
 \* 38125: gap of unknown length  
 \* 38225: gap of unknown length  
 \* 38226: contig of 1549 bp in length  
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 \* 39875: contig of 1180 bp in length  
 \* 41055: gap of unknown length  
 \* 41155: contig of 1679 bp in length  
 \* 42834: gap of unknown length  
 \* 42934: contig of 1234 bp in length  
 \* 44168: gap of unknown length  
 \* 44268: contig of 1179 bp in length

Query Match 24 1%; Score 158 4; DB 2; Length 142388;  
 Best Local Similarity 93 4%; Pred. No. 2; e-26; Length 142388;  
 Matches 198; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

QY 2 ATGGCTTCACTCTGACCTTCGCTCTGGAGCCACCTGGCTCGTGCCTGCCCCGGCCCTCTT-CCCTCTT 61  
 Db 74013 ATGACTTCACTCTGACCTTCGCTCTGGAGCCACCTGGCTCGTGCCTGCCCCGGCCCTCTT-CCCTCTT 74070  
 QY 62 GGCCCTTCTAGGCCGCCAGCTTCCTGCGCTGCGTGTGATGCCGCCAGGGCGCCGACCGC 121  
 Db 74071 GGCCCTCCAGGCCGCCAGCTTCCTGCGTGTGATGCCGCCAGGGCGCCGACCGC 74130  
 QY 122 CCCGCTCTGGCTGCCGCCAGGGCGCCGCCCCCTGTTGGTAACTGGAA 181  
 Db 74131 CCCGCTCCCTGCCCCGGTGGCCGAGGCCGCCGGTGGCCGAGGTCAACTGG 74130  
 QY 182 GTCATTAAGCTGGAATGAGAGAGGGTT 213  
 Db 74191 ATGA-AGAACCGCTGGAATGAGAGAGGGTT 74221



source 1. .984  
 BASE COUNT 206 a /organism="unknown"  
 ORIGIN 319 c 265 g 194 t

Query Match 13.2%; Score 85.4; DB 6; Length 984;  
 Best Local Similarity 66.8%; Pred. No. 1.1e-09;  
 Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 214 TGTGGTGTGAAAGGGCTTCGGTACTACTGACCATCGGCCCTCGGGCTTG 273  
 Db 5 TGGATGGACCCGGCTGCGATGGCTGCTACACAGAGCTCTCATCGCA 184  
 Qy 274 GCTCATGACCATCGGCCATCACACTGACTACTGACCATCGGCCCTCGGGCTTG 273  
 Db 65 CGCTCATGCCATGCCATGCCACGACTACGGCTGCTACAGCGGCACATCGCA 124  
 Qy 334 ACACCAACACTCACGAGGATGGAGGACCCATGTGGGCACTGGCCT 393  
 Db 125 ACGGCACCAACCTGACCATGGAGGACCCATGTGGGCACTGGCCT 393  
 Qy 394 CCGA 397  
 Db 185 CCCA 188

Search completed: February 9, 2003, 19:41:17  
 Job time : 2927 secs

RESULT 15  
 AX101260 AX101260  
 LOCUS AX101260  
 DEFINITION Sequence 1 from Patent WO0121791. 984 bp DNA linear  
 ACCESSION AX101260  
 VERSION AX101260.1 GI:13620050  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Buterlia; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 984)  
 AUTHORS Clare,J.J., Plimpton,M., Moss,F.J. and Sanseau,P.  
 TITLE Stargazin-like neuronal Ca2+-channel gamma subunit polypeptides  
 PATENT: WO 0121791-A 1 22-MAR-2001;  
 GLAXO GROUP LIMITED (GB)

FEATURES location/Qualifiers

source 1. .984  
 /organism="Homo sapiens"  
 /db\_xref="Taxon:9606"  
 /note="unnamed protein product"  
 /protein\_id="CAC36505\_1"  
 /db\_xref="GI:13620051"  
 /translation="MVRCDRLQMLLTAGAAFAFSIMATAIGTDWLYSSAHICNGT  
 NLTMDDCPPRARRGDLTHSIWRVCCXXGKHKHPRINIFPDMDYDHSSEYLLR  
 ITRASSVFPPISTILLLGGIGAGRIVSKYKNNTVLSAGILFVAGLSNITIGIYT  
 SSNTGCPSPDKDEDKHNHYNGWSFFGALSIVATVVAVNTIEKNEKELRFTK  
 RFLKASSSSPYARMSYRYRRRSKSSRSRTEASPSRDVPMGLKLTGAPMGEIS  
 VTLSPRLKVTAAASPDQDASFLWDFQDLSREGFHSMLNRRTPV"  
 BASE COUNT 204 a 319 c 265 g 194 t 2 others

ORIGIN  
 Query Match 13.2%; Score 85.4; DB 6; Length 984;  
 Best Local Similarity 66.8%; Pred. No. 1.1e-09;  
 Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 214 TGTGGTGTGAAAGGGCTTCGGTACTACTGACCATCGGCCCTCGGGCTTG 273  
 Db 5 TGGATGGACCCGGCTGCGATGGCTGCTACACAGAGCTCTCATCGCA 184  
 Qy 274 GCTCATGACCATCGGCCATCACACTGACTACTGACCATCGGCCCTCGGGCTTG 273  
 Db 65 CGCTCATGCCATGCCATGCCACGACTACGGCTGCTACAGAGCTCTCATCGCA 124  
 Qy 334 ACACCAACACTCACGAGGATGGAGGACCCATGTGGGCACTGGCCT 393



OM nucleic - nucleic search, using sw model  
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## SUMMARIES

AI991.DAT:*	AI991.DAT:*
AI993.DAT:*	AI992.DAT:*
AI994.DAT:*	AI995.DAT:*
AI996.DAT:*	AI997.DAT:*
AI998.DAT:*	AI999.DAT:*
AZ2000.DAT:*	AZ2001A.DAT:*
AZ2001B.DAT:*	AZ2002.DAT:*
e to have a t being printed, ution.	
-----	
Description	
-----	
DNA encoding a vol	
Human capping CDNA.	
CDNA encoding mous	
Oligonucleotide fo	
Oligonucleotide fo	
DNA encoding a vol	
Human voltage gate	
Human membrane cha	
CDNA encoding mous	
-----	
PH	Key
FT	CDS
FT	1..984
FT	/tag= a
XX	/product= "voltage-gated calcium channel"
PN	WO20014224-A1.
XX	
PD	16-MAR-2000.
XX	
PF	06-SEP-1999;
XX	99WO-GB02944.
PR	08-SEP-1998;
XX	98GBB-0019592.
PA	(SNIK ) SMITHKLINE BEECHAM PLC.

Score No. 13 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## ALIGNMENT

XX	Duckworth DM, Hayes PD;	PT	GLAXO ) GLAXO GROUP LTD.
DR	WPI; 2000-256976/22.	PA	
DR	P-PSDB; AAV84372.	XX	
XX	Isolated voltage-gated calcium channel polypeptide, designated CACNLIKE3, to treat diseases such as neurological disorders, epilepsy, neurodegenerative disorders, cognitive disorders and cancer; comprises 327 amino acid sequence -	PT	
PS	Claim 4; Page 31; 37pp; English.	XX	
XX	The present sequence encodes a human skeletal muscle voltage-gated calcium channel polypeptide, designated CACNLIKE3. The CACNLIKE3 polypeptide and polynucleotide are useful in the treatment of diseases such as neurological disorders, epilepsy, stroke, head trauma, migraine, affective disorders including depression and anxiety, schizophrenia, neurodegenerative disorders including Alzheimer's disease, cognitive disorders, types of pain and cancer. The polynucleotide is also valuable for chromosome localisation studies. The CACNLIKE3 polypeptide and polynucleotide are also useful in diagnostic assays for detecting diseases associated with inappropriate CACNLIKE3 activity or levels.	CC	
XX	Sequence 984 BP; 206 A; 319 C; 265 G; 194 T; 0 other;	CC	
CC	Query Match 13.2%; Score 86.4; DB 21; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 214 TGTGGGTTGAAAGGGCTTCAGGACTACTGCTTACACCATCGCGCCCTCGGGCTTTG 273 Db 5 TCCGATGCGACGGGGCTTCAGATGCTGCTGACCGACCTCTGACCGCCGAGCCCTCGCGCC 64	CC	
CC	Query Match 13.2%; Score 86.4; DB 21; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 274 GGCTCATGGCATCGCCATCAGCACTGACTCTACAGAGCTCATCGCA 333 Db 65 CGCTCATGGCATCGCCATCGCATCGCCACTACTGGCTGACTCCAGCGACATCGCA 124	CC	
CC	Query Match 13.2%; Score 86.4; DB 21; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 334 ACACCAACCTCACGAGGTATGAGCGACCACCCATGTGGGGCAGTGGCTCT 393 Db 125 AGGGCACCAACCTGACCATGGACGACGGGCCCCGGCCGGGACCTCA 184	CC	
CC	Query Match 13.2%; Score 86.4; DB 21; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 394 CCGA 397 Db 185 CCCA 188	CC	
XX	Sequence 984 BP; 204 A; 319 C; 265 G; 194 T; 2 other;	CC	
CC	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 214 TGTGGGTTGAAAGGGCTTCAGGACTACTGACCCACATGGGGCTTCGCGGCTTTG 273 Db 5 TCCGATGCGACGGGGCTTCAGATGCTGCTGACCGCCGAGCCCTCGCCCTCT 64	CC	
CC	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 274 GGCTCATGACCATCGCCATCAGCCTGTACTACTGGCTTACACAGAGGTCTCTTGCA 333 Db 65 CGCTCATGGCATCGCCATCGGACCGACTACTGGTGTACTCCAGCGCCACATCTGCA 124	CC	
CC	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 334 ACACCAACCTCACGAGGTATGAGCGACCACCCATCGGGGGCAGTGGCTCT 393 Db 125 AGGGCACCAACCTGACCATGGACGACGGGCCCCGGCCGGCCGGCACCTCA 184	CC	
CC	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 394 CCGA 397 Db 185 CCCA 188	CC	
XX	RESULT 2	XX	
XX	AAF81301 AAF81301 standard; cDNA; 984 BP.	XX	
XX	AC AAF81301;	XX	
DT	01-JUN-2001 (first entry)	XX	
XX	DE Human Cacng8 cDNA.	XX	
XX	KW Human; stargazin-like; CACNG8; anticonvulsant; hypotensive; vasotropic; antiarrhythmic; antianginal; analgesic; trophotropic; cytostatic; neuroprotective; cerebroprotective; antidiabetic; antimigraine; antiarteriosclerotic; immunosuppressive; antiparkinsonian; auditory; opthalmological; tranquiliser; neuronal disorder; calcineurin channel modulation; ss.	XX	
XX	OS Homo sapiens.	XX	
XX	PN WO200121791-A2.	XX	
PD	29-MAR-2001.	XX	
PF	25-SEP-2000; 2000WO-GB03685.	XX	
PR	23-SEP-1999; 99GB-0022571.	XX	
XX	PI Clare JJ, Plumpton M, Moss FJ, Sanseau P;	XX	
XX	DR WPI; 2001-266074/27.	XX	
XX	P-PSDB; AAB73979.	XX	
XX	PT Novel stargazin-like polypeptides capable of modulating the steady state inactivation of an alpha1 pore-forming subunit of a voltage-gated calcium channel, for treating central nervous system disorders -	XX	
XX	PT calcium channel, for treating central nervous system disorders -	XX	
XX	PS Claim 6; Page 38-39; 48pp; English.	XX	
XX	The present sequence is provided in a specification relating to an isolated stargazin-like polypeptide comprising a sequence of 327 or 275 amino acids fully defined in the specification, or its variant capable of modulating the steady state. The polypeptide is useful for treating a subject having a neuronal disorder that is responsive to calcium channel modulation. It is useful in the manufacture of a medicament for treatment or prophylaxis of a disorder that is responsive to calcium channel modulation, e.g. epilepsy, episodic ataxia, spinocerebellar ataxia, hypertension, ischaemic heart disease, arrhythmia, angina, pain, cerebral ischaemia, Alzheimer's disease, neuroprotection, stroke, diabetes, cerebral vasospasm, atherosclerosis, tardive dyskinesias, peripheral vascular disease, immunosuppression, cancerous diseases, migraine, headache, bipolar disorder, unipolar depression, anxiety, Parkinson's disease, cognitive disorders, ophthalmic diseases, neuromuscular disorders and tinnitus. Nucleic acids encoding these polypeptides are useful in the production of the polypeptides, and as primers.	CC	
XX	Sequence 984 BP; 204 A; 319 C; 265 G; 194 T; 2 other;	CC	
XX	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 214 TGTGGGTTGAAAGGGCTTCAGGACTACTGACCCACATGGGGCTTCGCGGCTTTG 273 Db 5 TCCGATGCGACGGGGCTTCAGATGCTGCTGACCGCCGAGCCCTCGCCCTCT 64	CC	
XX	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 274 GGCTCATGACCATCGCCATCAGCCTGTACTACTGGCTTACACAGAGGTCTCTTGCA 333 Db 65 CGCTCATGGCATCGCCATCGGACCGACTACTGGTGTACTCCAGCGCCACATCTGCA 124	CC	
XX	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 334 ACACCAACCTCACGAGGTATGAGCGACCACCCATCGGGGGCAGTGGCTCT 393 Db 125 AGGGCACCAACCTGACCATGGACGACGGGCCCCGGCCGGCCGGCACCTCA 184	CC	
XX	Query Match 13.2%; Score 86.4; DB 22; Length 984; Best Local Similarity 66.8%; Pred. No. 1e-12; Matches 123; Conservative 0; Mismatches 61; Indels 0; Gaps 0; Oy 394 CCGA 397 Db 185 CCCA 188	CC	
XX	RESULT 3	XX	
XX	ABK51915 ID ABK51915 standard; cDNA; 1071 BP.	XX	
XX	AC ABK51915;	XX	
XX	DT 13-AUG-2002 (first entry)	XX	
XX	DE cDNA encoding mouse Cacng4.	XX	
XX	KW Mouse; neuronal voltage-gated calcium channel gamma subunit; epilepsy; immunosuppressive; anticonvulsant; Cacng4; gene; ss.	XX	
XX	OS Murinae gen. sp.	XX	
FT	KEY Location/Qualifiers	XX	
FT	5-UTR 1..21	XX	







PR	12-NOV-1998;	98US-0191283.	PT	/*tag= c
PR	09-DEC-1998;	98US-0208821.	XX	
PR	26-JAN-1999;	99US-0237506.	PN	US6365337-B1.
PR	10-FEB-1999;	99US-0247891.	XX	
XX			PD	02-APR-2002.
PA			XX	
XX			PF	27-JUL-1998;
PT	Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yue H;	98US-0123030.	XX	
PT	Lal P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzai Y;	27-JUL-1998;	PR	98US-0123030.
XX			XX	
WPI:	2000-256643/22.		PA	{ IOWA } UNIV IOWA RES FOUND.
DR			PA	(JACK) JACKSON LAB.
XX			XX	
PS	Novel human membrane channel protein and polynucleotide useful for diagnosing and treating cell proliferative, inflammatory, secretory, osmoregulatory, muscular, cardiovascular and neurological disorders -		PT	Letts VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;
XX			XX	
CC	Claim 9; Page 126; 140pp; English.		PT	WPI; 2002-433421/46.
CC			DR	P-PSDB; AAU97134.
CC	The present sequence is a cDNA identified in Incyte clone 1267774 derived from BRAIN09 cDNA library. It encodes human membrane channel protein-12 (MECHP-12), which is expressed in nervous tissues. Anti-MECHP antibodies can be used as therapeutic antagonists and reagents for diagnosis and monitoring diseases. MECHP cDNA can be used for diagnosis of MECHP-related diseases and gene mapping. MECHP can be used for treatment of cell proliferative disorders such as bursitis and atherosclerosis, cancers like lymphoma and sarcoma, inflammatory disorders like AIDS and Addison's disease, transport/secretory disorders like cystic fibrosis and diabetes mellitus, osmoregulatory disorders like diarrhoea and renal failure, muscular disorders like myocarditis and Duchenne's muscular dystrophy, cardiovascular disorders like hypertension and vasculitis, congenital lung anomalies like bronchitis and neurological disorders like Alzheimer's disease, Parkinson's disease and Huntington's disease.		XX	
CC			PS	Novel nucleic acid sequences encoding a neuronal voltage-gated calcium channel gamma subunit useful in screening for compounds which modulate activity of the channel and in diagnosing, treating neuronal diseases
CC			XX	
CC	Disclosure; FIG 6; 36pp; English.		PT	
CC			XX	The present invention relates to the isolation of mouse genes encoding neuronal voltage-gated calcium channel gamma subunits designated Cacng2, Cacng3, and Cacng4. The genes are useful for identifying candidate compounds for modulating the activity of human neuronal voltage-gated calcium channels. They are also useful for diagnosing and treating the autoimmune disease Lambert-Eaton syndrome, as well as diagnosing defects in gamma subunit genes of a patient with a neuronal disease such as epilepsy. The present sequence encodes mouse Cacng3.
CC			XX	
CC	Sequence 1478 BP; 374 A; 416 C; 339 G; 349 T; 0 other;		PT	
CC			XX	
CC	Query Match 8.3%; Score 54.4; DB 21; Length 1478; Best Local Similarity 70.2%; Pred. No. 0.0025; Matches 73; Conservative 0; Mismatches 31; Indels 0; Gaps 0;		PT	
CC			XX	
CC	QY 218 GTGTGAAAAGGGTTCAGGTACTACTGACCACATGGGCCCTGGGCCCTTGCCCT 277		PT	
Db	372 GTTGATGAGGTTCAAATGCTTAAACACCGTGCTCTGCCTCAGCCT 431		XX	
Db			PT	
QY	278 CATGACCACGCCATCAGCAGTACTACTGCTCTCACAGAGAG 321		XX	
Db	432 GATGACCATAGCTGGAAACCGACTATGGCTCTACTCCAGAG 475		PT	
CC			XX	
CC	Sequence 1477 BP; 352 A; 449 C; 356 G; 320 T; 0 other;		PT	
CC			XX	
CC	Query Match 8.2%; Score 53.6; DB 24; Length 1477; Best Local Similarity 66.4%; Pred. No. 0.004; Matches 77; Conservative 0; Mismatches 39; Indels 0; Gaps 0;		PT	
CC			XX	
CC	QY 218 GTGTGAAAAGGGTTCAGGTACTACTGACCACATGGGCCCTGGGCCCTTGCCCT 277		PT	
Db	496 GTGTGACAGGATTCAGATGTTCACTACTGTTAGGACCTCGCACTTTAGTT 555		XX	
Db			PT	
QY	278 CATGACCACGCCATCAGCAGTACTACTGCTCTCACAGAGAG 321		XX	
Db	556 ANTGACCATAGCTGGACGGACTACTGCTATATCCAGAGGTGTCCAGGA 611		PT	
CC			XX	
CC	RESULT 9		PT	
ABK51914			ABK51913	
ID	ABK51914 standard; cDNA; 1477 BP.		ID	ABK51913 standard; cDNA; 1558 BP.
XX			XX	
AC	ABK51914;		AC	ABK51913;
XX			XX	
DT	13-AUG-2002 (first entry)		DT	13-AUG-2002 (first entry)
XX			XX	
DE	CDNA encoding mouse Cacng3.		DE	CDNA encoding mouse Cacng2.
XX			XX	
Mouse; neuronal voltage-gated calcium channel gamma subunit; autoimmune disease; Lambert-Eaton syndrome; neuronal disease; epilepsy; immunosuppressive; anticonvulsant; Cacng3; gene; ss.			KW	Mouse; neuronal voltage-gated calcium channel gamma subunit; autoimmune disease; Lambert-Eaton syndrome; neuronal disease; epilepsy; immunosuppressive; anticonvulsant; Cacng2; gene; ss.
OS	Murinae gen. sp.		OS	Murinae gen. sp.
XX			XX	
PH	Key Location/Qualifiers		PH	Key Location/Qualifiers
PT	5'UTR 1..487		PT	5'UTR 1..389
PT	/*tag= a		PT	/*tag= a
PT	488..1435		PT	390..1361
CDS	/*tag= b		CDS	/*tag= b
PT	/product= "Cacng3"		PT	/product= "Cacng2"
PT	3'UTR 1436..1477		PT	1362..1558
XX			XX	

/\*tag= PN WO200014225-A1.

XX XX PD 16-MAR-2000.

XX XX PF 06-SEP-1999; 99WO-GB02945.

XX XX PR 08-SEP-1998; 98GB-0019589.

XX XX PA (SMK ) SMITHKLINE BEECHAM PLC.

XX XX PI Duckworth DM, Hayes PD;

XX XX DR WPI; 2000-256977/22.

XX XX P-PSDB; AAY84375.

XX XX PT CACNLIKE polynucleotides and polypeptides, useful in diagnostic assays and for treating conditions such as Alzheimer's -

XX XX PS Claim 11; Page 31; 33pp; English.

XX XX CC The present sequence represents an expressed sequence tag (EST) corresponding to a putative human neuronal voltage-gated calcium channel gamma-2 and gamma-3 subunits, designated CACNLIKE2 polypeptides. The CACNLIKE2 polynucleotide and polypeptide are useful for treating neurological disorders, epilepsies, stroke, head trauma, migraine, affective disorders including depression and anxiety, schizophrenia, neurodegenerative disorders including Alzheimer's disease, cognitive disorders, pain and cancer. They may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA in cells. The polypeptides may also be used as vaccines to induce an immunological response in mammals.

XX XX SQ Sequence 945 BP; 232 A; 274 C; 217 G; 222 T; 0 other;

XX XX SQ Query Match 7.9%; Score 52; DB 21; Length 945; Best Local Similarity 65.5%; Pred No. 0.00091; Matches 76; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

XX XX Qy 218 GTCGAAAGGGCTCAGGTACTACTGACCCACATGGCGCTCCGGCTTGGCT 277

XX XX Db 9 GTGAGCAGAGGTATCCAGATGTTGATCACCAGTAGGCTTGGCTTGTAGTT 68

XX XX Qy 278 CATGACCATGCCATCAGACTGACTACTGGCTCTACACAGGCTCTCATCTGCA 333

XX XX Db 69 ATGACCATGGCAGGGACTACTGGTTATTCAGGGTGTGCGAGGA 124

XX XX Db 458 GATGACCATGCCCTGGGAAACGGACTATGGCTTACCTCCAGAG 501

RESULT 11

AAZ9794 ID AAZ9794 standard; DNA; 945 BP.

XX AC AAZ9794;

XX DT 12-JUL-2000 (first entry)

XX DE EST corresponding to a neuronal voltage-gated calcium channel DNA.

XX DE Human; neuronal voltage-gated calcium channel; gamma-2 subunit; gamma-3 subunit; CACNLIKE2; neurological disorder; epilepsy; stroke; head trauma; migraine; affective disorder; depression; anxiety; schizophrenia; neurodegenerative disorder; Alzheimer's disease; cognitive disorder; pain; cancer; vaccine; expressed sequence tag; EST; ss; Homo sapiens.

XX OS Homo sapiens.

Location/Qualifiers 1..945 /\*tag= a /product= "voltage-gated calcium channel"

XX FH Key CDS

XX FT FT

XX PN WO200014225-A1.

XX XX PD 16-MAR-2000.

XX XX PR 27-JUL-1998; 98US-0123030.

XX XX PA (IOWA ) UNTV IOWA RES FOUND.

XX XX PA (JACK- ) JACKSON LAB.

XX XX PR Letts VA, Frankel WN, Campbell KP, Felix R, Biddlecome G;

XX XX DR WPI; 2002-433421/46.

XX XX P-PSDB; AAU97153.

XX XX PS Claim 2; Fig 2; 36pp; English.

XX XX CC The present invention relates to the isolation of mouse genes encoding neuronal voltage-gated calcium channel gamma subunits designated Cacng2, Cacng3, and Cacng4. The genes are useful for identifying candidate compounds for modulating the activity of human neuronal voltage-gated calcium channels. They are also useful for diagnosing and treating the autoimmune disease Lambert-Eaton syndrome, as well as diagnosing defects in gamma subunit genes of a patient with a neuronal disease such as epilepsy. The present sequence encodes mouse Cacng2.

XX XX SQ Sequence 1558 BP; 418 A; 441 C; 360 G; 339 T; 0 other;

XX XX SQ Query Match 8.0%; Score 52.8; DB 24; Length 1558; Best Local Similarity 69.2%; Pred No. 0.00066; Matches 72; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

XX XX Qy 398 GTGAGCAGAGGTATCCAGATGTTGATCACCAGTAGGCTTGGCTTGTAGTT 457

XX XX Db 278 CATGACCATGCCATCAGACTGACTACTGGCTCTACACAGGCTCTCATCTGCA 321

RESULT 12

AAZ9793 ID AAZ9793 standard; DNA; 948 BP.

XX AC AAZ9793;

XX DT 12-JUL-2000 (first entry)

XX DE DNA encoding a neuronal voltage-gated calcium channel.

XX DE Human; neuronal voltage-gated calcium channel; gamma-2 subunit; gamma-3 subunit; CACNLIKE2; neurological disorder; epilepsy; stroke; head trauma; migraine; affective disorder; depression; anxiety; schizophrenia; neurodegenerative disorder; Alzheimer's disease; cognitive disorder; pain; cancer; vaccine; ss.

XX OS Homo sapiens.

Location/Qualifiers 1..948 /\*tag= a /product= "voltage-gated calcium channel"

XX FH Key CDS

XX FT FT

XX PN WO200014225-A1.

XX XX PD 16-MAR-2000.



ID	AAC77216 standard; cDNA; 1854 BP.							
XX								
AC	NACT7216;							
XX								
DT	08-FEB-2001 (first entry)							
XX								
DE	Human ORF8 ORF2771 polynucleotide sequence SEQ ID NO:5541.							
XX								
KW	Human; open reading frame; ORF8; detection; cytostatic; hepatotropic; vulnery; antipsoratic; anti-parkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressive; immunostimulant; thrombolytic; coagulant; vasotrophic; anti-diabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; hypertension; antianemic; gen therapy; cancer; proliferative disorder; neuroprotective; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; infection; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malacia; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; coagulation; thrombosis; contraceptive; ss.							
XX								
OS	Homo sapiens.							
XX								
PN	WO20058473-A2.							
XX								
PD	05-OCT-2000.							
XX								
PF	31-MAR-2000; 2000WO-US08621.							
XX								
PR	31-MAR-1999; 99US-0127607.							
PR	02-APR-1999; 99US-0127636.							
PR	05-APR-1999; 99US-0127728.							
PR	30-MAR-2000; 2000US-0540763.							
PA	(CURA-) CURAGEN CORP.							
XX								
PI	Shimkets RA, Leach M;							
XX								
DR	WPI; 2000-602362/57.							
DR	P-PDB; AAB43307.							
XX								
PT	Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -.							
XX								
PS	Claim 5; Page 474-4725; 550pp; English.							
XX								
CC	AAC7446 to AAC77605 encode the proteins given in AAB40237 to AAB43397, which represent the human ORF8 open reading frames 1 to 3161. The ORF8 sequences have activities such as: cytostatic; hepatotropic; vulnery; antipsoratic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressive; immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiflammatory; antibacterial; antiviral; antirheumatic; antithyroid; and antianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORF8-associated disorder. The nucleic acids can be used to express ORF8 proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.							
XX								
SQ	Sequence 1854 BP; 460 A; 549 C; 414 G; 429 T; 2 other;							
XX								
Query	Match	7.9%; Score 52; DB 21; Length 1854;						
Best	Local	Similarity	65.5%; Pred. No. 0.0011;					
Matches	76;	Conservative	0; Mismatches	40;	Indices	0;	Gaps	0;
Db	354	GTGTGACAGAGGTATCCAGATGTTGATCAGCTTGTGAGGCTTGTGGCTTTAGTT	277					
Qy	278	CATGACCATGCCATCAGACTGACTGACCTATGGCCCTTGGGCTTTGGCC	333					
Db	414	AATGACCATGCACTGGGACAGGACTACTGGTATATTGAGGCTGAGGAGGA	469					
RESULT	15							
AAV55831/C								
ID	AAV55831 standard; DNA; 799 BP.							
XX								
AC	AAV55831;							
XX								
DE	18-NOV-1998 (first entry)							
XX								
DE	Nucleotide sequence of the stabilising sequence-encoding insert.							
XX								
PF	Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; kappaB regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition; ss.							
XX								
OS	Epstein-barr virus.							
XX								
PN	WO9822577-A1.							
XX								
PD	28-MAY-1998.							
XX								
PF	17-NOV-1997; 97WO-1B01508.							
XX								
PR	25-JUN-1997; 97US-0048945.							
PR	15-NOV-1996; 96US-0030986.							
XX								
PA	(MASU/) MASUCCI M G.							
XX								
PI	Masucci MG;							
XX								
DR	WPI; 1998-312463/27.							
XX								
PT	New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence containing glycine repeats							
XX								
PS	Disclosure; Fig 4B; 120pp; English.							
XX								
CC	This is a nucleotide sequence of the stabilising sequence-encoding CC insert. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or CC inserting onto or into the core protein a stabilising polypeptide of CC sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, CC Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need not CC be identical from n repeat to n repeat. Alternatively a nucleic acid CC encoding the stabilising polypeptide can be linked onto or inserted into CC a nucleic acid encoding a core protein. The fusion proteins of the CC invention are more resistant to degradation by proteases and, thus, have CC a longer half-life than the unfused core protein. The products can be CC used for treating autoimmune diseases, cancer and inflammation. In CC particular, the core protein may be an kappaB regulator protein for the CC treatment of inflammatory bowel disease, or a nitroreductase protein CC which can activate nitro drugs in enzyme/prodrug therapy to treat cancer CC or other pathological conditions. The fusion proteins can also be used in CC diagnostic methods such as in vivo imaging.							
XX								
SQ	Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;							

Query Match 6.5%; Score 42.8; DB 19; Length 799;  
Best Local Similarity 58.7%; Pred. No. 0.21; Mismatches 0;  
Matches 74; Conservative 0; Indels 0; Gaps 0;  
Qy 13 CTGACCTTCGCTCTGCAGCACCTGCCTGCCCCGGCCCTCTGACCCCTTGAG 72  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 740 CTGACCTTCGCTCTGCCTGCCTCCCTGCCCCGGCCCTCTGACCCCTTGAG 681  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 73 GCCCCAGCTCTGCTGTGCTGATCCCCAACCGCGGGCACGGCCGCCCGC 132  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 680 CCCCTCTGCTCTGCCCCCTCTGCCCCCTCTGCTGCCCCCTCTGCTGCTG 621  
||| |||  
Qy 133 TGCCCC 138  
|||  
Db 620 CTGCC 615

Search completed: February 9, 2003, 18:52:19  
Job time : 229 secs

- Sequence 41, Appl
- Sequence 16, Appl
- Sequence 12835, A
- Sequence 1, Appl
- Sequence 33, Appl
- Sequence 292, Appl
- Sequence 529, App
- Sequence 3950, App
- Sequence 2321, App
- Sequence 29, Appl
- Sequence 1, Appl
- Sequence 45, Appl
- Sequence 45, Appl
- Sequence 16, Appl
- Sequence 16, Appl
- Sequence 4, Appl
- Sequence 50, Appl
- Sequence 50, Appl
- Sequence 50, Appl
- Sequence 2164, App
- Sequence 1601, App
- Sequence 59, Appl



US-09-944-413-41

Query Match Similarity 61.1%; Score 39.8; DB 9; Length 1377; Best Local Similarity 56.5%; Pred No. 0.17; Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

b	359	CCTGGCTGCCA	349
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ESOL# 4  
S-09-944-403-41/c

Sequence 41, Application US/09944403  
PATENT NO. US2002165143A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Boiststein, David  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillian, Kenneth  
APPLICANT: Kjelvin, Ivar  
APPLICANT: Nepliar, Mary  
APPLICANT: Roy, Margaret  
APPLICANT: Tunas, Daniel  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
FILE REFERENCE: P2568P1CI  
CURRENT APPLICATION NUMBER: US/09/944,403  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 09/066,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/067,411  
PRIOR FILING DATE: December 3, 1997  
PRIOR APPLICATION NUMBER: 60/069,334  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,335  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,278  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,425  
PRIOR FILING DATE: December 12, 1997  
PRIOR APPLICATION NUMBER: 60/069,696  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,694  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,702  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,870  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/069,873  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/069,017  
PRIOR FILING DATE: December 18, 1997  
PRIOR APPLICATION NUMBER: 60/070,440  
PRIOR FILING DATE: January 5, 1998  
PRIOR APPLICATION NUMBER: 60/074,086  
PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/075,945  
PRIOR FILING DATE: February 25, 1998  
PRIOR APPLICATION NUMBER: 60/112,850  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 60/113,296  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 60/146,222  
PRIOR FILING DATE: July 28, 1999  
PRIOR APPLICATION NUMBER: PCT/US98/19330  
PRIOR APPLICATION NUMBER: PCT/US98/25108  
PRIOR FILING DATE: December 1, 1998  
PRIOR APPLICATION NUMBER: 09/16,021  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 09/218,517  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 09/254,311  
PRIOR FILING DATE: March 3, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: June 22, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: September 15, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28409  
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28301  
PRIOR FILING DATE: December 1, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: December 16, 1999  
PRIOR APPLICATION NUMBER: PCT/US00/03565  
PRIOR FILING DATE: February 11, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: February 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: March 2, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/08439  
PRIOR FILING DATE: March 30, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/114042  
PRIOR FILING DATE: May 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: July 28, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: December 1, 2000  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: February 28, 2001  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 41  
LENGTH: 1377  
TYPE: DNA  
ORGANISM: Homo Sapien  
09-944-403-41

Query Match: 6.1%; Score: 39.8; DB: 9; Length: 1377;  
Best Local Similarity: 56.5%; Pred: 0.17; Mismatches: 57; Indels: 0; Gaps: 74; Conservative: 0; Mismatches: 57;

37 CTGCTCGCTGCCCCCGGCCCTCTGGCCCTTGAGGCCCTGGCTCTGCTCTGCTGCTG 96  
479 CTCTCTCGCGGCCGGGGTCCCTCTGAGGCTCCCGCAGTCCCGCCCTCCGGCTCTCGCTT 420

97 TGATCCCCCAAGGCCGCCACGGCCGGCCCTCGCTGCCCCGGTGGTGGCCACGCC 156  
419 TCTCTCCCGAGGCCGGCGCCGCTGCGCCGGCTGGCCATCGGGCCGGCAAGC 360  
157 CCCGGTGC 167  
359 CCTGGCTGCCA 349

## RESULT 5

US-03-944-896-41/c  
 ; Sequence 41, Application US/09944896  
 ; Patent No. US20020168715A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Kljavin, Ivar  
 ; APPLICANT: Napier, Mary  
 ; APPLICANT: Roy, Margaret  
 ; APPLICANT: Tumas, Daniel  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P2548P1  
 ; CURRENT APPLICATION NUMBER: US/09/944,896  
 ; CURRENT FILING DATE: 2001-08-31  
 ; PRIOR APPLICATION NUMBER: 09/866,028  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/069,334  
 ; PRIOR FILING DATE: December 11, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,335  
 ; PRIOR FILING DATE: December 11, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,425  
 ; PRIOR FILING DATE: December 12, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,696  
 ; PRIOR FILING DATE: December 16, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,694  
 ; PRIOR FILING DATE: December 16, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,702  
 ; PRIOR FILING DATE: December 16, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,870  
 ; PRIOR FILING DATE: December 17, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,873  
 ; PRIOR FILING DATE: December 17, 1997  
 ; PRIOR APPLICATION NUMBER: 60/068,017  
 ; PRIOR FILING DATE: December 18, 1997  
 ; PRIOR APPLICATION NUMBER: 60/070,440  
 ; PRIOR FILING DATE: January 5, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,086  
 ; PRIOR FILING DATE: February 9, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,092  
 ; PRIOR FILING DATE: February 9, 1998  
 ; PRIOR APPLICATION NUMBER: 60/075,945  
 ; PRIOR FILING DATE: February 25, 1998  
 ; PRIOR APPLICATION NUMBER: 60/112,850  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 60/113,296  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 60/145,222  
 ; PRIOR FILING DATE: July 28, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330  
 ; PRIOR FILING DATE: September 16, 1998  
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108  
 ; PRIOR FILING DATE: December 1, 1998  
 ; PRIOR APPLICATION NUMBER: 09/215,021  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 09/218,517  
 ; PRIOR FILING DATE: December 2, 1998  
 ; PRIOR APPLICATION NUMBER: 09/254,311  
 ; PRIOR FILING DATE: March 3, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999

RESULT 6  
 US-03-944-944-41/c  
 ; Sequence 41, Application US/09944944  
 ; Patent No. US20020173463A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Kljavin, Ivar  
 ; APPLICANT: Napier, Mary  
 ; APPLICANT: Roy, Margaret  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Wood, William  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: NO. US20020168715A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: NO. US20020168715A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: December 16, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565  
 ; PRIOR FILING DATE: February 11, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: February 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: March 2, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439  
 ; PRIOR FILING DATE: March 30, 2000  
 ; PRIOR FILING DATE: May 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710  
 ; PRIOR FILING DATE: July 28, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: December 1, 2000  
 ; PRIOR FILING DATE: February 28, 2001  
 ; PRIOR FILING DATE: February 28, 2001  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SEQ ID NO: 41  
 ; LENGTH: 1377  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-03-944-896-41

Query Match 6.1%; Score 39.8; DB 9; Length 1377;  
 Best Local Similarity 56.5%; Pred. No. 0.17; Mismatches 57; Indels 0; Gaps 0;  
 Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy	37	CTGCAGCGCTCCCGGCGCCCTCTGGCCCTTGAGGCCCGCAGCTCTGGCCCTGGCAG 96
Db	479	CTCCCTCGCGCCCGGGTCCTCTGAGGTCCTCCGGCAGTCCTCCGGCTCCCGGCTGGCC 420
Qy	97	TGATCCCCAGCCCCGGGAGGGCCCGCTCCGCTGCCGGTGGTGGCCACGGCC 156
Db	419	TCTCTCCGGAGCCCGGGGGCGCTGGGGCCATCGCCGCCCGCAAGC 360
Qy	157	CCGGGTTGCCA 167
Db	359	CTGGCTGCCA 349





PRIOR FILING DATE: 1997-11-07  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065846  
 PRIOR FILING DATE: 1997-11-17  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
 PRIOR APPLICATION NUMBER: 60/066453  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/066511  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/069212  
 PRIOR FILING DATE: 1997-12-11  
 PRIOR APPLICATION NUMBER: 60/069278  
 PRIOR FILING DATE: 1997-12-11  
 PRIOR APPLICATION NUMBER: 60/069334  
 PRIOR FILING DATE: 1997-12-11  
 PRIOR APPLICATION NUMBER: 60/069694  
 PRIOR FILING DATE: 1997-12-16  
 PRIOR APPLICATION NUMBER: 60/072320  
 PRIOR FILING DATE: 1998-01-23  
 PRIOR APPLICATION NUMBER: 60/073612  
 PRIOR FILING DATE: 1998-02-04  
 PRIOR APPLICATION NUMBER: 60/074086  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: 60/074092  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: 60/077791  
 PRIOR FILING DATE: 1998-03-12  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079663  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079728  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/080165  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/081203  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081229  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081695  
 PRIOR FILING DATE: 1998-04-14  
 PRIOR APPLICATION NUMBER: 60/081817  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081818  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082999  
 PRIOR FILING DATE: 1998-04-24  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/083545  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084637  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085149  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085338  
 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15

Query Match

Best Local Similarity 6.1%; Score 39.8; DB 9; Length 1377;  
 Matches 74; Conservative 0; Mismatches 57; Indexes 0; Gaps 0;

QY	37	CTGCTGCTGCCCGGCCCTCTGCCCCCTTGAGGCCCGCCAGCTTGCCCTGCTG 96
QY	479	CTCTCGGGCCGGGGTCCCTCGAGGCCGGCTCCGGCTCCGGCTTGCCCT 420
QY	97	TGATCCCCAGCCCCGACGCCCGCCGCTGCCGCTGGGCGCCAGGCCAGGCC 156
Db	419	TCTCTCCGGAGCCGGCGGCCGCTCGGCCATGCCAGGCCAGGCC 360
QY	157	CCGGTTGCCA 167
Db	359	CCTGCTGCCA 349

RESULT 10

US-10-121-049-361/C

; Sequence 361, Application US/10121049

; Publication No. US2003022239A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Bersini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Flivarooff, Ellen

; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey

; ORGANISM: Homo Sapier  
US-10-123-904-361

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watson, Colin K.

Query Match 6.1%; Score 39.8; DB 9; Length 1377;  
 Best Local Similarity 56.5%; Pred. No. 0.17;  
 Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0.

QY 37 CTCGCTCGTGCCCCGGCCCCCTGCCCCCTGAGGCCAGCTCTGCGCTGCG 96

APPLICANT: Zhang, Zenlin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C17  
CURRENT APPLICATION NUMBER: US10/121,049  
CURRENT FILING DATE: 2002-04-12  
Prior Application removed - See File Wrapper or Palm

ORGANISM: Homo Sapiens  
US-10-121-049-361

US-10-140-470-361/c  
; Sequence 361, Application US/1014047  
; Publication No. US20030023311

Best Local Similarity 56.5%; Pred. No. 0.17; Mismatches 57; Indels 0; Gaps 0

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Mauree  
APPLICANT: DeForge, Laura

APPLICANT: Stewart, Timothy A  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K

RESULT 11  
US-10-123-904-361/c

APPLICANT: Zhang, zemi  
TITLE OF INVENTION: SEC

RESULT 11  
US-10-123-904-361/c  
; Sequence 361, Application US/10123904  
; Publication No. US20030022328A1  
; GENERAL INFORMATION:

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
FILE REFERENCE: P2330R1C160  
CURRENT APPLICATION NUMBER: US/10/140,470

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresin, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Flivarcot, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gritten, Mary E.  
APPLICANT: Goddard, Audrey

; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION REMOVED - SEE PAIN OR FILE WRAPPER  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 361  
LENGTH: 1377  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-470-361

APPLICANT: Godowski, Paul J.  
APPLICANT: Sherney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria

Query Match	6.1%;	Score 39.8;	DB 9;	Length 1377;
Best Local Similarity	56.5%;	Pred. No. 0.17;		
Matches	74;	Conservative	0: Mismatches	57: Indices 0: Gaps

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanae, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

QY	37	CTGCTCTGCCCCGCCCCCTGCGCCCTTGAGGCCCGAGCTTCGCTGTGCTG	96
Db	479	CTCTCGGCCCCGGGGTCCCTCGAGGTCCGGAGTCCGGCTTCCCGCCCTGCGCT	420
QY	97	TGATCCCCCAGCGGGGGAGGGCCCGGCTCCGCTGCCCGGGTGGCCACGGCC	156

; FILE OF INVENTION: ACTOS ENCODING THE SAME  
; FILE REFERENCE: P3320R1C5A  
; CURRENT APPLICATION NUMBER: US10/123,904

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Db
419  TCTCTCCGGAGCCCCGGGAGCCCTGCGGCCGCGGCCATCGCGCCCGCAAGG  360

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CURRENT FILING DATE: 2002-04-16  
PRIOR APPLICATION removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 361

## RESULT 1



PRIOR APPLICATION NUMBER: PCT/US00/20710  
 PRIOR FILING DATE: July 28, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/32678  
 PRIOR FILING DATE: December 1, 2000  
 PRIOR APPLICATION NUMBER: PCT/US01/05520  
 PRIOR FILING DATE: February 28, 2001  
 NUMBER OF SEQ ID NOS: 120  
 SEQ ID NO 41  
 LENGTH: 1377  
 TYPE: DNA  
 ORGANISM: Homo Sapien

US-09-944-449-41

Query Match 6.1%; Score 39.8; DB 10; Length 1377;  
 Best Local Similarity 56.5%; Pred. No. 0.17; Mismatches 0; Gaps 0;  
 Matches 74; Conservative 0; Indels 0; Gaps 0;

OY 37 CTGCTGGCTGCCCGCCCGCCCTCTGGCCCTTGAGCCCCCAAGCTCTGCCCTGTG 96  
 Db 479 CTGCTGGCTGCCCGCCCGCCCTCTGGCCCTTGAGCCCCCAAGCTCTGCCCTGTG 420

OY 97 TGTATCCCCAGCCGGCAAGGCCGCTCCACTGCCCGCTGAGCTGGTGGCCCTAGGCC 156  
 Db 419 TCTCTCCGGAGCCCCGGCCCTCGGGCGCTGCGGCCATCGGGCCCCGGAAGC 360

OY 157 CCCGGTTGCCA 167  
 Db 359 CCTGGCTGCCA 349

RESULT 15

US-09-944-457-41/c

; Sequence 41, Application US/09944457  
 ; Patent No. US0020110859A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Allen  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Kljavin, Ivar  
 ; APPLICANT: Napier, Mary  
 ; APPLICANT: Roy, Margaret  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Wood, William  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P2548PIC1  
 CURRENT APPLICATION NUMBER: US/09/944,457  
 CURRENT FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: 09/866,028  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/067,411  
 PRIOR FILING DATE: December 3, 1997  
 PRIOR APPLICATION NUMBER: 60/069,334  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,335  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,278  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,425  
 PRIOR FILING DATE: December 12, 1997  
 PRIOR APPLICATION NUMBER: 60/069,696  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,694  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,702  
 PRIOR FILING DATE: December 18, 1997  
 PRIOR APPLICATION NUMBER: 60/070,440  
 PRIOR FILING DATE: January 5, 1998  
 PRIOR APPLICATION NUMBER: 60/074,086  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/074,992  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/075,945  
 PRIOR FILING DATE: February 25, 1998  
 PRIOR APPLICATION NUMBER: 60/112,850  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: September 9, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: December 1, 1998  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 15, 1998  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/254,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 22, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/24409  
 PRIOR FILING DATE: NO. US20020108591ember 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/20313  
 PRIOR FILING DATE: NO. US20020108591ember 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21301  
 PRIOR FILING DATE: December 1, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/3095  
 PRIOR FILING DATE: December 16, 1999  
 PRIOR APPLICATION NUMBER: PCT/US00/0565  
 PRIOR FILING DATE: February 11, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/0414  
 PRIOR FILING DATE: February 22, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/05841  
 PRIOR FILING DATE: March 2, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/08439  
 PRIOR FILING DATE: March 30, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/14042  
 PRIOR FILING DATE: May 22, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/24710  
 PRIOR FILING DATE: July 28, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/32678  
 PRIOR FILING DATE: December 1, 2000  
 PRIOR APPLICATION NUMBER: PCT/US01/05520  
 PRIOR FILING DATE: February 28, 2001  
 NUMBER OF SEQ ID NOS: 120  
 SEQ ID NO 41  
 LENGTH: 1377  
 TYPE: DNA  
 ORGANISM: Homo Sapien

US-09-944-457-41

Query Match 6.1%; Score 39.8; DB 10; Length 1377;  
 Best Local Similarity 56.5%; Pred. No. 0.17; Mismatches 0; Gaps 0;  
 Matches 74; Conservative 0; Indels 0; Gaps 0;

OY 37 CTGCTGGCTGCCCGCCCGCCCTCTGGCCCTTGAGCCCCCAAGCTCTGCCCTGTG 96  
 Db 479 CTGCTGGCTGCCCGCCCGCCCTCTGGCCCTTGAGCCCCCAAGCTCTGCCCTGTG 420

Qy	97	TGATCCCCCGGAGCCCCGGAGGGGCCGCTCCGCTGCCGCTGCCACGGCC	156
Db	419	TCTCTCCGGAGGCCGGGGGGGCCGCTGCCGCTGCCGCTGCCAG	360
		TGGGGCCGGAA	

Search completed: February 9, 2003, 20:10:03  
Job time : 66 secs



GenCore version 5.1.3  
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On nucleic - nucleic search, using sw model.  
Run on: February 9, 2003, 18:46:59 ; Search time 1931 Seconds  
(without alignments) 1 cell updates/sec

Title: US-10-060-066-2  
Perfect score: 656  
Sequence: 1 tatcggttactctgtcacct.....tggtaaaaaattttttttg 656  
5501.936 Million cell updates/sec

Scoring table: IDENTITY\_NUC  
Searched: Gapop 10.0, Gapext 1.0  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*

2: em\_esthun:\*

3: em\_estin:\*

4: em\_estinu:\*

5: em\_estov:\*

6: em\_estol:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_lestom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pnt:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rnd:\*

Minimum DB seg length: 0  
Maximum DB seq length: 200000000

7 102.2 15.6 983 17 CNS0489W  
8 86.4 13.2 600 12 BG03929  
9 81.8 11.5 594 13 BI981765  
10 81.4 12.4 587 13 BE844628  
11 74.4 11.3 999 17 CNS04NDM  
12 73.6 11.2 691 13 BG912818  
13 73.2 11.2 592 17 FR019468  
14 62 9.5 615 17 CNS04174  
15 61.4 9.4 687 17 CNS04LQ0  
16 61.4 9.4 688 10 BE212599  
17 61.4 9.4 697 10 BE774164  
18 56 8.5 923 17 CNS012DK  
19 54.4 8.3 575 17 FR019451  
20 54.4 8.3 580 10 BE222518  
21 54.4 8.3 599 9 AI912567  
22 53.4 8.1 965 13 BI457751  
23 54.4 8.3 640 10 BE670632  
24 54 8.2 1043 17 CNS03MBE  
25 53.6 8.2 649 14 BM051619  
26 53.6 8.2 855 13 BT739481  
27 53.4 8.1 157 9 AI93801  
28 53.4 8.1 965 13 BI457751  
29 52.8 8.0 477 12 BE611331  
30 52 7.9 739 13 BI53438  
31 52 7.9 757 13 BI821976  
32 52 7.9 763 13 BT53725  
33 52 7.9 775 12 BE705097  
34 52 7.9 788 13 BI546513  
35 52 7.9 872 13 BI821441  
36 52 7.9 890 13 BI544699  
37 52 7.9 1080 17 AQ93056  
38 52 7.9 1938 11 BC033741  
39 50.8 7.7 710 17 AQ689558  
40 50.4 7.7 436 17 B50198  
41 49.8 7.6 776 17 CNS010RY  
42 49.8 7.6 844 17 CNS052P  
43 49.8 7.6 887 14 B029511  
44 49.8 7.6 971 17 AG079392  
45 49.6 7.6 641 9 AI357868

## ALIGNMENTS

RESULT 1  
BEG47856 BEG47856  
LOCUS BEG47856 337 bp mRNA linear EST 06-SEP-2000  
DEFINITION UI-M-BHL-anh-C-12-0-UI.r1\_NtSC\_BMAP\_MS2 Mus musculus cDNA clone  
UI-M-BHL-anh-C-12-0-UI 5', mRNA sequence.  
ACCESSION BEG47856  
VERSION BEG47856.1 GI:9973676  
KEYWORDS EST:  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (base 1 to 337)  
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 9704477  
COMMENT

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	332.4	50.7	337 10	BEG47856
C	234.2	35.7	558 10	BB647956 UI-M-BHL- B0266161 NTSC_ff1
C	180.6	28.9	547 10	BB102334 UI-R-BTL
C	174	26.5	245 12	BB864111 UI-M-BHL- BB864111 UI-M-BHL- BB641732 BB641732
C	159.8	24.4	663 10	BB641732 BB641732
C	155.8	23.8	472 10	AW060348
				AW060348 UI-M-BHL-

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9543, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mES@nih.gov  
DNA Library Preparation: M.B. Soares Lab Clone distribution:  
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It  
should be noted that Bento Soares is generating a small number of  
additional specialized non-redundant arrays of BMAP cDNAs whose

availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence: 88-148, >GC-rich#low\_complexity Seq primer: M13 Reverse.

## FEATURES source

1. .337  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-BH1-anth-c-12-0-UI"  
/clone\_id="NIH\_BMAP\_M\_S2"  
/dev\_stage="Z7-32 days"  
/lab\_host="Dil0B (Life Technologies)"  
/note="vector: pRT3D-pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The NIH\_BMAP\_M\_S2 library is a subtracted library derived from NIH\_BMAP\_M\_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones obtained from the NIH\_BMAP\_M\_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."  
BASE COUNT 56 a 128 c 86 g 67 t  
ORIGIN

Query Match Similarity 50.7%; Score 332.4; DB 10; Length 337;  
Best Local Similarity 99.7%; Pred. No. 1.6e-66;  
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 ACCCTGGCCCTGAGCCACTGCTGGCGCCCCGGCCCTCTGGCCCTGAGGCC 76  
Db 4 ACCCTGGCCCTGAGCCACTGCTGGCGCCCCGGCCCTCTGGCCCTGAGGCC 63

Qy 77 CCCAGCTCTGCCCTGCTGATGCCAGCCCGGACGCCCCGGCTCTGGCTGTC 136  
Db 64 CCCACCTCTGCCCTGCTGATGCCAGCCCGGACGCCCCGGCTCTGGCTGTC 123

Qy 137 CGCGAGGTGSSGCCACGGCCCGCCGGTGGCAGTGAACTGGAGTCATGAAACGCG 196  
Db 124 CGGGTGTGGCCACGGCCCGGGTGGCTGAGTCATGAAACGCGTCATGGCTGAGCTG 183

Qy 197 GAACTGAGAGAGGCTTCTGGGTGAAAGGGGTCTAGTACTGACCACATGG 256  
Db 184 GAACTGAGAGGCTTCTGGGTGAAAGGGGTCTAGTACTGACCACATGG 243

Qy 257 CGCCCTGCGGCTTGGCTCATACCATGGCATGAGCTACTGGCTTACAC 316  
Db 244 CGCCCTGCGGCTTGGCTCATACCATGGCATGAGCTACTGGCTTACAC 303

Qy 317 AAGGACTCTCATCTGCAACACCAACCTGACA 350  
Db 304 AAGGACTCTCATCTGCAACACCAACCTGACA 337

## RESULT 2

BO266161/c  
LOCUS BO266161 558 bp mRNA linear EST 07-MAY-2002  
DEFINITION NSC\_ff1c05\_x1 NEI\_CGAP\_Manus Mus musculus cDNA clone IMAGE:2665416  
3', mRNA sequence.

ACCESSION BO266161  
VERSION BO266161.1  
KEYWORDS EST  
SOURCE house mouse.

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 558)

REFERENCE 1  
NCF-CGAP http://www.ncbi.nlm.nih.gov/ncicbap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgbps\_r@mail.nih.gov

TISSUE PROCUREMENT Lothar Hennighausen/Robin Humphreys  
CDNA LIBRARY PREPARATION: Life Technologies

CDNA Sequencing Center (NSC) Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

MG:1046188 Plate: LLAM069 row: F column: 9  
Seq primer: -2M13 forward primer (ABI).

FEATURES source  
1. .558

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:2855416"  
/clone\_id="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="Dil0B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: Sali; Site\_2: NotI; Cloned unidirectionally. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

## RESULT 3

BE102334/c  
LOCUS BE102334 547 bp mRNA linear EST 13-JUN-2000  
DEFINITION UI-R-B1-aql-d-02-0-UI.s1 UI-R-B1 Rattus norvegicus cDNA clone

ACCESSION BE102334  
VERSION BE102334.1  
EST BE102334.1 GI:8494433  
SOURCE Norway rat.

ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (bases 1 to 547)

REFERENCE 1  
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene

FEATURES	source	VERSION	BB864111.1
		KEYWORDS	GI:10384829
COMMENT		SOURCE	EST.
		ORGANISM	house mouse
CONTACT: Soares, MB		REFERENCE	I. (bases 1 to 245)
Program for Rat Gene Discovery and Mapping		AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.
University of Iowa		TITLE	Discovery
451 Eckstein Medical Research Building Iowa City, IA 52242, USA		JOURNAL	Genome Res. 6 (9), 791-806 (1996)
Tel: 319 335 8250		MEDLINE	9704477
Email: mssoares@blue.weeg.uiowa.edu		COMMENT	Contact: Chin, H
The sequence tag present in the cDNA between the NotI site			National Institute of Mental Health
and the oligo-dT track served to identify it as a clone from the			6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
normalized corpus-striatum library. Library Preparation: M.B.			20892-6643, USA
Soares Lab Clone distribution: clones will be available through			Tel: 301 443 1705
Research Genetics (www.resgen.com) The following repetitive			Fax: 301 443 9890
elements were found in this cDNA sequence: 147-294, >B3#SINE/B2			Email: mEST@mail.nih.gov
SEQ PRIMER: M13 Forward			CDNA Library Preparation: M.B. Soares lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
FEATURES	source	SEQ PRIMER	M13 Reverse
		Location/Qualifiers	1. . 245
1. . 547			
/organism="Rattus norvegicus"			
/strain="Sprague-Dawley"			
/db_xref="txon:0116"			
/clone_id="UI-R-BT1-aql-3-02-0-01"			
/dev_stage="adult"			
/lab_host="DH10B (Life Technologies)"			
/note="Vector: pTT3D-Pac (Pharmacia) with a modified			
polylinker; Site,1: Not I; Site,2: Eco RI; The library			
UI-R-BT1 is a subtracted library derived from a mixture of			
the following tissues: hippocampus, thalamus, mid-brain,			
medulla, corpus striatum, cerebellum, cortex and testis. For			
a detailed description of the library from which this			
clone was derived, please visit our Web site at:			
arest.engr.uioawa.edu. The subtraction has been previously			
described in (Bonaldo, Lennon and Soares, Genome Research			
6,791-806, 1996)			
TAG_LIB=UI-R-BT1			
TAG TISSUE="corpus-striatum"			
TAG_SEQ="CTAGG"			
BASE COUNT			
150 a 148 c 121 g 128 t			
ORIGIN			
• Query Match 28.9%; Score 189 6; DB 10; length 547;			
Best Local Similarity 90.5%; Pred. No. 1.3e-33;			
Matches 209; Conservative 0; Mismatches 21; Indels 1; Gaps 1;			
BASE COUNT			
39 a 67 c 77 9 61 t 1 others			
ORIGIN			
• Query Match 26.5%; Score 174; DB 12; Length 245;			
Best Local Similarity 99.4%; Pred. No. 5.3e-30;			
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
BASE COUNT			
663 a 663 c 663 9 663 t 1 others			
ORIGIN			
• Query Match 663 bp mRNA linear EST 29-SEP-2000			
Best Local Similarity 99.4%; Pred. No. 5.3e-30;			
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
BASE COUNT			
663 a 663 c 663 9 663 t 1 others			
ORIGIN			
RESULT 4			
BB64111/c			
LOCUS BB864111			
DEFINITION UT-M-B11-anp-a-08-0-UT.R1 NIH_BMAP_M_S2 Mus musculus cDNA clone			
ACCESSION BB864111			
RESULT 5			
BB641732			
LOCUS BB641732			
DEFINITION RIKEN full-length enriched, 10 days neonate cortex Mus			
ACCESSION BB641732			



JOURNAL	freshwater pufferfish Tetraodon nigroviridis
REFERENCE	Unpublished (bases 1 to 983)
AUTHORS	Genoscope.
TITLE	Direct Submission
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .
FEATURES	/organism="tetraodon nigroviridis" /db_xref="taxon:9983" /clone="09615" /clone_1.lib="G" /note="Genoscope sequence ID : COBG090AD08LPL1-end : T7" /Location/Qualifiers
BASE COUNT	216 a 305 c 254 g 202 t 6 others
ORIGIN	1. .983
Query Match	15.6%; Score 102.2; DB 17; Length 983;
best local Similarity	67.5%; Pred. No. 1.8e-13;
Matches	168; Conservative 0; Mismatches 63; Indels 18; Gaps 1;
QY	214 TGTGGTGGAAAGGGCGTCAGGTACACTGACCACATGGGGCTTCGGGCTTGT 273
Db	293 TGTGGTGGACGGGGCAGCTCAGGTCTCACCCATGGGGCTTGTGAGCTTCG 352
QY	274 GCCCTCATGACCATGCCATCAGACTGACTACTGCTCATACAGAGACTCATCTCA 333
Db	353 CCCGTATGAGGGTGGCCATCGGACCGACTACTGCTTACGCTGCGCTTCACTCGCA 412
QY	334 ACACCCACACCTCACAGGGATGAGGGACCCATCTGGGGCAGTGGCTCT 393
Db	413 ACACGACGCGCAACTCCACCCAGACAGAC-----TCCAACAGCAACA 454
QY	394 CCGAGAGAGGACCCCTGGGGCTCACACATCACGGCTCTGGGGATATGCTGCCAG 453
Db	455 AAGCACAGGAGGACCCGGGCCCTACCCACTGGGCTCTGGAGGATCTGCTGCCAG 514
QY	454 AAGTAGGG 462
Db	515 AAGGTACGG 523
RESULT 7	
INS0489W	CNS0489W
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 09615 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	AL279005
ORGANISM	Tetraodon nigroviridis.
KEYWORDS	Tetraodon nigroviridis.
FEATURES	Tetraodon nigroviridis.
REFERENCE	Bukarvata; Metzoco; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
AUTHORS	Roest-Croilius H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
REFERENCE	1 (bases 1 to 983)
AUTHORS	Unpublished (bases 1 to 983)
JOURNAL	Roest-Croilius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
REFERENCE	2 (bases 1 to 983)
AUTHORS	Charpentier and repeat analysis of the compact genome of the
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
FEATURES	
BASE COUNT	138 a 106 g 103 t
ORIGIN	125 c 106 g 103 t
Query Match	23.8%; Score 115.8; DB 10; Length 472;
best local Similarity	85.5%; Pred. No. 8.1e-26;
Matches	177; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
QY	450 CTGGAAGCTAGGTGCGAAGGCCCTGGTGCACCTCCGAGCTGCGCTINCA 509
Db	472 CTGGAAAGGTAGGTCGAGAACGCCCTGGTGCACCTCCGAGCTGCGCTTCA 413
QY	510 GCAATCGACTTNTAGTGTCTGAGTCACACCAAGGNCCTGAGGGGTGCTTACTG 569
Db	412 GCAATCGACTTCTAGTCTGAGTCACACCAAGGCTGAGGGGTGCTTACTG 353
QY	570 CTGGAGGGGNTATTCATGACCCCTGACAGCTTCTGGGG 629
Db	352 CTGGAGGGGTGATTCATGACCCCTGACAGCTTCTGGGGAT 294
QY	630 TTTTNGNGTTATTCTTATTCTTG 656
Db	293 TCTCGTTTATTTTATTTACTGG 267
RESULT 8	
INS04929	BG803929
DEFINITION	600 bp mRNA sequence.
ACCESSION	BG803929
VERSION	BG803929.1
KEYWORDS	EST.
ORGANISM	Mouse
REFERENCE	Bukarvata; Metacora; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 600)
AUTHORS	Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., White, R.A., Bernand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
TITLE	Gene expression in the developing mouse retina by EST sequencing and microarray analysis
REFERENCE	Nucleic Acids Res. 29 (24), 4983-4993 (2001)
JOURNAL	21671825
COMMENT	Contact: Klein, WH
FEATURES	Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA Tel: 713 792 3646 Fax: 713 790 0329. Location/Qualifiers 1. .600





Best Local Similarity 65.4%; Pred. No. 7e-07; 64; Indels 1; Gaps 1;		LOCUS		CNS04174	
Matches 123; Conservative 0; Mismatches 1;		DEFINITION		Tetraodon nigroviridis genome survey sequence T7 end of clone 11104 of library G from Tetraodon nigroviridis, genomic survey sequence.	
QY	211 GRTGTTGCTGTTGAAAAAGGGCGTTCAGGACTACTGACCAACATGGGCCCTTGGCGGCTT 270	ACCESSION	AI291865		
Db	4 GGGCTGTGATCGACCCGGGGCTGCAGATCTGGCTGGACCGACGGCGGCCCTGGCGGCT 63	VERSION	AL291865.1	GI:8030445	
QY	271 TTGGCTCATGACCATGCCATCAGACTGACTGGCTTACAGAGGCTCTCATCT 330	KEYWORDS	GSS: genome survey sequence.		
QY	64 TCTCGCTCATGGCCATGCCATGGGACCGACTGGCTTACCCGGCGCAC 123	SOURCE	Tetraodon nigroviridis.		
Db	64 GCAAC-ACCAACCAACCTCACAGCAGGTATGACGGACCCATCGTGGGGCAGTGGC 389	ORGANISM	Tetraodon nigroviridis		
QY	124 GCACTGGGACCAACCTGACCATGGACGAGGGCCCCGGCCCCGGAC 183	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.		
QY	390 TCTCCGA 397	AUTHORS	Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quétier, F., Saurin, W. and Weissenbach, J.		
Db	184 CTCACCCA 191	TITLE	Tetraodon nigroviridis		
QY	RESULT 13	JOURNAL	Unpublished		
Db	FR0019468	REFERENCE	(bases 1 to 615)		
QY	DEFINITION F.rubripes GSS sequence, clone 029J13bd4, genomic survey sequence.	AUTHORS	Bouneau, L., Billault, A., Quétier, F., Saurin, W., Bernot, A. and Weissenbach, J.		
Db	ACCESSION AL012359	TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis		
QY	VERSION AL012359.1	JOURNAL	Unpublished		
Db	GSS: genome survey sequence.	REFERENCE	(bases 1 to 615)		
QY	SOURCE TakiFugu rubripes	AUTHORS	Genoscope.		
Db	ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; TakiFugu.	FEATURES	Direct Submission		
QY	REFERENCE 1 (bases 1 to 392)	JOURNAL	Submitted (12-APR-2000)		
Db	AUTHORS Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.	COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, Please take a look at <a href="http://www.genoscope.cnrs.fr/tetraodon">http://www.genoscope.cnrs.fr/tetraodon</a> .		
QY	TITLE Direct Submission	FEATURES	1. .615		
Db	JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biolhelp@hgmmp.mrc.ac.uk	COMMENT	/organism="Tetraodon nigroviridis"		
QY	COMMENT Vector: phBlueScript II KS	FEATURES	/db_xref="taxon:99883"		
Db	PRIMER: V-type: phagemid	COMMENT	/clone="11104"		
QY	DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.	FEATURES	/clone_11104="G"		
Db	FEATURES source	COMMENT	/clone_11104="G"		
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Db	FEATURES source	ORIGIN	130 a 162 c 187 g 130 t 6 others		
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Db	FEATURES source	ORIGIN	130 a 162 c 187 g 130 t 6 others		
QY	Query Match 9.5%; Score 62; DB 17; Length 615;	Query Match	9.5%; Score 62; DB 17; Length 615;		
Db	Best Local Similarity 63.3%; Pred. No. 0.00033; 2; Mismatches 78; Indels 12; Gaps 4;	Best Local Similarity	63.3%; Pred. No. 0.00033; 2; Mismatches 78; Indels 12; Gaps 4;		
QY	Matches 159; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	Matches	159; Conservative 0; Mismatches 78; Indels 12; Gaps 4;		
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Db	341 TGTGGCTGAGGGCGCATCCGGCTGCTGCCACCGCTGGAGCTTGCAGCTTC 282	QY	273 GGCCTATGACCATCCCATAGCA-CTGACTACTGCTCACACAGAGCTCTAC 331		
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Db	341 TGTGGCTGAGGGCGCATCCGGCTGCTGCCACCGCTGGAGCTTGCAGCTTC 282	QY	332 CACACACCCACCTCACAGGAGCTGGGGCGTCACACATTGAGCCCTTGCGGAGTATGCTCCT 391		
QY	341 TGTGGCTGAGGGCGCATCCGGCTGCTGCCACCGCTGGAGCTTGCAGCTTC 282	Db	221 CAACACCA-CGCCCCCTCTCCACCTCACAGGAGCTCAACACGCMATCTATAGTACA- 165		
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QY	276 CTCGACCATGCCATCACACTGACTCTGCTCACACAGAGCTTCATCTGCAAC 335	Db	164 -----AGAAGGACCTGGGGACCTTACCGACTGGCTCTGAGGTTCTGCCT 112		
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QY	146 CTGATNACTATGCCATGGACCTACTGGCTCTATTCGGGGCGTACATCTGCAAT 205	Db	111 GGTAGTACGG 101		
Db	336 ACCACCAACCTCACAGCAGGTA 358				
QY	206 ACCACCAACCTCACACCGGAGCA 228				

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RS004174/CNS04174/CNS04174/QQ Locus 687 bp DNA linear GSS 21-MAY-2000

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DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 119E09 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AI296159

VERSION AI296459.1 GI:8035039

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM Tetraodon nigroviridis.

REFERENCE 1 (bases 1 to 687)

AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Acanthomorphia; Acanthopterygii; Percomorphia; Tetraodontiformes; Actinopterygii; Metacara; Chordata; Craniata; Vertebrata; Euteleostomi; Euteleostei; Neoteleostei; Teleostei; Neoteleostei; Tetraodontidae; Tetraodon.

REFERENCE 2 (bases 1 to 687)

AUTHORS Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quétier, F., Saurin, W. and Weissenbach, J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 687)

AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billebaut, A., Quétier, F., Saurin, W., Bernot, A. and Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 687)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.ens.fr/Tetraodon>.

FEATURES

SOURCE

1. - 687

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BASE COUNT

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ORIGIN

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Db 156 GTTCGACCCGGAGTCAGAWGCTGCTGACMAGTGGGCCCTTCGCCCTTCAGCT 215

Qy 278 CATTGACCATGCGCATCAGCACTACTAGGCTCTACACAAGGCTCATCGCAACAC 337

Db 216 CATTGACCATGCGCATGGGACGCACTACTGGCTGCTGCGGGTGTGCCAGGACAA 275

Oy 338 CACCA 342

Db 276 GGCA 280

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